Amendments to the Specification:

Please replace Table 1, beginning on page 8, line 10, with the following amended Table 1.

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Marker Name	Sequence	SEQ ID NO
1-85/5B5/86-1	AGCAAGCTTACATGCGTGGA[GT/AA]GAGAGTCCTCGAGATCAACC	30
2-85/5B12/N3-1	CCTTGATCTCTCAAGTAATC[A/G]TCTCACCGGAAGATCCCTGA	31
3-85/5C3/86-2	ACCATCCATTAAACTGTATC[A/G]TCGCAATCTAACCAAAAGTT	32
4-85/5E1/86-1	TAAAGCAAAGAGAGTCTTAC[C/A]GTCTGCTGCATGATATACCC	33
5-85/5E1/86-2	CTACTGATAGTGAACCACCC[A/C]ATCCCCAAATTTAAAGCAAA	34
6-85/6A11/86	ATCCTATTGGTAGTAACACA[G/A]ATTGAGTTAATGTTGCAGGG	35
7-N1/6A11/N2	AGGCAAAGCGGGTAGTTGCAA[G/A]ACTGCTTCTCACGAGGTAAT	36
8-N1/6A9/N2-1	CCAGCTTCAATGTCTGCATG[C/A]TTGTGTCGATGCCAAAGTTC	37
9-N1/6A9/N2-2	AAAGTTCATTACGATGATCT[A/G]ACCCTGCAGTCATCCATGGA	38
10-85/6A12/86	CTTCCCCCCCTCAATACCTC[T/G]TTCAAAAGTGAAAAGTGCAG	39
11-N1/6D1/N2-1	ATTTTGTTTGTTTCTTGTC[G/C]GGTCAGGTCAGAACAAAGTT	40
12-N1/6H5/N2	AAACCAGAGCCACCTCCTTA[C/]CCACCTCATCGTTCCTTTC	41
13-86/6F11/N2-2	GATTTCGACCGCAGTCTCAC[G/T]GAGGATGAGTATATCGCTTT	42
14-N1/6F11/N2	TAGGACAGGCAAACAATCTA[C/A]GCGGTCAAAATCCGATTTCG	43
16-N1/8B5/N2	ACTCAAAAAAACGATACCTC[G/C]GCCGTCTCTCGCCGTCTCGC	44
17-N1/8D4/N2-1	CAGGAGACAGTTACAGTCCC[/A]CAGAGTCGCAAGGATCTCGAA	45
18-85/8D4/86-2	CTGATCTTGAAGGAGAGACC[A/G]CCACAAGGTTCCATCCTATG	46
19-85/8H11/86	AGTGCgAGGCTCAGTTGGAT[G/T]ATTAGGGTGTCAGTAAATCA	47
20-85/10B8/86	NAGGTCCATGATGATGACAA[T/A]AAAGGTATTCCACATGTCAA	48
21-N2/10B8/N3-2	ACATCCAACTTTCTCCCAGT[T/C]CTTTATTCTATCCTGATTTG	49
21-N2/10B8/N3-2	ACATCCAACTTTCTCCCAGT[T/C]CTTTATTCTATCCTGATTTG	50
22-N2/10B8/N3-1	AAGGTATTCCATTGGTATAC[A/C]TCCAACTTTCTCCAGTTCT	5051

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23-85/10B9/86	GACCCTTCTTGGGAAAGAAAG[T/C]TGTAACCGGCGTCGAGATTCG	5152
24-10C8/N2	ATAGAAACCGCCGATGCTCA[A]GGACACGCCACCGTCTTCGT	5253
25-10C8/N2	CACTTTCTTCGTGGCTAAAT[T]CTTCGGCCGAGCGGTCTCA	5354
26-10D2/N1	GTTATCATCAGTACCGGTAT[T]AACCCCAAGGCTAATTCTTA	5455
27-85/10D2	TTGGGTATCTACGGACTGAT[C]ATCGCTGTTATCATCAGTAC	5556
28-N1/10E12/N2-1	GGAATTCAATACTCGCCAAC[G/T]TCTTCATTGCTGTCGTCGGC	5657
29-N1/10E12/N2-2	TCCTTACGCCTTCAAGCGCA[C/G]CGGCTGGCTCATGGGTGTCC	5758
30-N1/10F4/N2	TGTATCTATGCGGTGGCTGC[G/C]GTCTCCGTTCGCGCCAGTAC	5859
31-10F4/N2	GCGCCAGTACCGCCGCCGGTTAC[A]ATCTCACTGCCTTCACGTCC	5960
32-85/10F4/N2	GCGCCAGTACCGCCGCCGGTTAC[G/A]ATCTTAATGCCTTCACGTTC	6061
33-85/10F9/N1-2	AACTTGGAATTCCACAACTT[G/C]AGAAACTTGATGTGGTGCC	6162
34-85/10F9/86	CGGTACTGCGAAAGCTGGAG[C/G]ATCAACTTGGAATTCCACAA	6263
35-86/10F12	AAAAGTGCTATTGTTCAGGT[G]GATGCTGCTCCGTTCAAGCA	6364
36-85/10H6/86	GTCAAAAGCCACGGATTCAA[G/A]AACGTGCTCTTCTTGCGCCT	6465
38-85/10F12/86	AAACCAGGGTCCTTGATGTG[T/]GTCTACAACGCTTCCAACAA	6566
39-85/11B7/86	AANACCCTGAGCTCATGCCT[C/T]TGACCCATGTTCTTGCCACC	6667
40-85/11C4/86	TTTGGGACCGTTGGAGTTGC[A/G]TCTGCGGCTATGACGGTGGA	6768
41-85/11D4/86-2	AATCTTTGCCATTGCTGTCA[A/G]TATCTTCGTCGCTTCAGCT	6869
43-N2/11D11/N3	GACAACGCTGGTGGTGTATTGC[C/T]GAAATGGCTGGAATGAGCCA	6970
44-86/11D11/N3	GCTGCTCTAGGGATGCTCAG[C/T]ACCATGCCACCGGTTTGGC	7071
45-85/11D11/86	ATGCTCAGCACCATCGCCAC[T/C]GGTTtGGCGATTGATGCTTA	7172
46-N2/11E3/N8a	GAGAAAGTGCTTGTGGAGAT[C/T]TACAaGTCCATACTGATGGC	7273
47-86/11E3/N2a	AATGCTTGTGGAGATtTACA[G/A]GTCCATACTGATGGCGCAGG	7374

48-86/11E3/N2b	AATGCTTGTGTGGAGATcTACA[G/A]GTCCATACTGATGGCGCAGG	7475
49-85/11F12/86	AATGATTGGTTTGAGAAGCA[T/A]ACAGCTGGTACGCTTGATAT	7576
50-85/11F7/86	GATAGGGCGAAGAGAGAGGAA[G/A]AGTCCTGAGAGAGGAAAGAGAT	7677
51-85/11H2/86-2	CTCTCTCTCCACAAAGACAC[A/C]GCTTTCTCCATGACCTTCGG	7778
52-85/11H5/86-2	TCTCTGACGTCATGAAAGCT[C/A]ATGGCAAAATTGCTGATGGA	7879
53-85/11H6/86-1a	GTTATCGATCGCGTGGTCCG[T/C]GAAACCCAAAATaCACCTTT	7980
54-85/11H6/86-1b	GTTATCGATCGCGTGGTCCG[T/C]GAAACCCAAAATtCACCTTT	8081
55-85/12B6/N3	CGTCAGCCTTCTTCCGCCGC[A/C]GTCGTCCTCCGCAACCGTGC	8182
56-86/12B6/85a	TGTCTCTTCCGTCAGCCTTC[C/T]TCCGCCGCAGTCGTCCTCCG	8283
57-86/12B6/85b	TGTCTCTTCCGTCAGCCTTC[C/T]TCCGCCGCGTCGTCCTCCG	8384
58-86/12B11/85	TCAGGTTTACCTCTATATAT[T/]ATATTCATGGTATGGAAGGT	8485
59-n1/12B11/N2-2	TATCCTGCAAATTGACATTT[T/C]CCTTCAGGTTCTAGAAGCTG	8586
60-85/12C2/86	CGAGAACAGAAGAGAAGAGA[C/]TGGAACACGTCGGACAGTAC	8687
62-12C11/N2	ACGGGTCCTAGCGCCATGGC[T]ATTTCCTCACCGTTTCTGG	8788
63-N1/12D10	TTGGGCTTTCGGTGGTATGA[T]CTTCGTCCTCGTCTATTGCA	8889
65-85/12F4/86-1	TCCTTGATTCCTTAATAATC[A/T]TTGGCTGGGGGTCTTTCTAA	8990
66-12G5/N1	GCTTGAATAACGATGTCTAC[T]CTGCCTCGGCGTACGGCGGA	9091
67-85/12G8	CTAAAAAGATCGACGAGTGT[C]CCTTACTACGCTCCATCTAT	9192
68-12G9/N1-1	AGGTGGGTTTAGCGTGGCAT[C]CGATCCATTGGATGGATCCA	9293
69-85/12G9/	NGTGGGTTTACCGTATCATT[T]GATCCATTGGATGGATCGAG	9394
70-12B11/N2-1	GCGGATCCTATATTGGGTCT[T]GATGGATTGTTTCTATCCCG	9495

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71 - /12B11/N2-2	TATCCTGCAAATTGACATTT [C] CCTTCAGGTTCTAGAAGCTG	~~95~~96
72 - N1/12E10	TACCACGGTCGTCGTACTGGTCG [A] TGTCTGGAACGTCACCAAGC	~~96~~97
73 - N1/13A3/N2a	CTGTCTCAgTTTGTTGGATC [C/G] AAATCgAATCGAAAGCGTAC	~~97~~98
74 - N1/13A3/N2b	CTGTCTCAgTTTGTTGGATC [C/G] AAATCaAATCGAAAGCGTAC	~~98~~99
75 - 13E8/N2	ACACTGTTGGAGGACGTGAA [G] AAGATATTCAAGACAACATC	~~99~~100
76 - N1/13F6/N2-2	TCTTTCGTATCTTGCTGAGT [C/T] GTTACGCCGTCAACACCCG	~~100~~101
77 - 13F8/N2-1	GGAACCCTAGGGAGCCCACA [G] CTCCTTATGCTAAGCGGCGT	~~101~~102
78 - 13F8/N2	GATCATAGTATCCGCCGGAA [C] CCTAGGGAGCCCACAGCTCC	~~102~~103
79 - 85/14B5/86	TTCGGCGGGTCGATCCGGGC [A/G] GAAGACATTGTCAGGTGANN	~~103~~104
80 - N1/14C2/N2	GCACCAACATTGTAAACCTA [T/G] AGCTTCTTCCTCAGCCACCT	~~104~~105
81 - 85/14C2/86-1	GCTGCCACATAGTGAACCTA [T/A] AGCTTCTTCCTCAGCCACCT	~~105~~106
82 - N2/14C2/85-2	GCACCAACATTGTGAACCTA [G/A] AGCTTCTTCCTCAGCCACCT	~~106~~107
83 - 85/14C2/86-2	AGTACATAGCTATTGACTAA [C/G] TTAAGTTCCTTGTATTGTTG	~~107~~108
84 - N2/14C2/85-1	CCTCTATCCGCCATGGTTGC [A/T] CCAACATTGTGAACCTAGAG	~~108~~109
85 - 85/14E2/86-2	TTGACCCTCGGCAAGCCACC [G/T] GTCAAGCCATGCTGCAGCCT	~~109~~110
86 - 85/14E2/86-1	AGGCTGCCCCTCTCCCAATTC [A/C] AAAGCCAACTCCTAAACCAA	~~110~~111
87 - 85/14E8/86	AAACATGGAAAGGCCTGATA [/G] TCACCGTCAAGCTCACCGTC	~~111~~112
88 - 85/14E12/86	CAACCTGAAAAATTGTTTTA [C/A] CAACGGCCCGCTTTCTCCA	~~112~~113
89 - 14H10/86	AAGGCCAACAACGACATTAC [C] TCCATCGTTAGCAACGGAGG	~~113~~114
90 - 85/14H10/86	TCACCGGCTTGAAGTCTTCC [G/T] CTGCATTCCCAGTCACCCGC	~~114~~115
91 - 85/15A6/86	ACTCAGCTTTCTTATGCCTC [G/] ACTTGCGACACACGAATCCA	~~115~~116

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92-85/15C4/86	TGCGGGCTAACATCTCTGGTG[G/T]TCACCTTAACCCAGCCGTAN	116117
93-85/15E5/86-1	CGAGGATCACTTCTCTCTGT[G/T]CAAGAAGAAGTTCGGCAAGG	117118
94-N1/15E5/N2-1	CTGTtCAAGAAGAAGTTCGG[C/T]AAGGTCTACGCTTCCCGCGA	118119
95-N1/15E5/N2-2	CCCTCTGCTCGTCACGGCGT[T/A]ACGCAGTTCTCGGATCTGAC	119120
96-86/15E5/N2	CCCGCGAGGAGCACGACTAC[A/T]GATTCTCCGTTTCAAATCC	120121
97-15E9/86	TCCACTCGCCGGGAAGAAAC[T]CGACAAACCGTTGTCTACTT	121122
98-15E9	ATGGCTCGCGACGGGTCTCC[G]GTAAACCTCGGAGAGCAGAT	122123
99-N2/15E9/86	GCCGACTCTCGAAGCTTCTT[A/]ACTCCACTCGCCGGGAAGAA	123124
100-85/15E9/86-1	GAATCTAGGAGAGCAGATCT[T/G]CCTCTCTATCTTCAATGTTC	124125
101-85/15E9/86-2	TCCACTCGCCGGGAAGAAAC[C/T]CGACAAACCGTTGTCTACAT	125126
102-N1/15E9/N2-1	GTCATGAAGATATTCACTAC[A/G]CCGACTCTCGAAGCTTCTTA	126127
103-85/15F1/86	GCAGGTAAAATTCTACAGAC[C/A]TTCCCTTTTCATTGTAGTTA	127128
104-85/15F5/86	TCTCCTCCGCGCGCAAGAA[G/A]AAATCGACACGGCGGCGTCT	128
105-85/15F10/86	GTGCCCTAAAGATACCCTCA[A/G]GCTTGGTGTCTGCGCTAATG	129
106-N2/15G1	TTCTTCCCACAGGTGAAACT[T]GCTAACTTCCTTCCAAAGTA	130
107-N1/15H7/N2	TATGTATCAGGACAATGTGT[GA/TT]GTGACTGTGGTTGCATCCAT	131
108-N1/16A1/N2-1	GCTAAGCTACGCAACTGCCA[C/T]CAATCAGGGCAAGCTAAAGG	132
109-85/16A5/86	TATACACTCTTTAAAAGCGT[G/C]TGTGTGTACCCATCTCTCTT	133
110-N1/16B6/N2	ATGGCTGCGTATTGGCTGTC[C/T]AAGGCTGGATCTTGGTCCCA	134
111-85/16B6/N1	GGATCCATCTCAACTATGGT[A/C]GTATTATCGTTGAGGCTAGG	135
112-85/16B7/86	GTATGTGATTCGGAAGAGAA[T/]CAAACTAAGTGCCGAGAAAG	136
113-N1/16D6/N2	GCTAAGGTAGTTGGAGGAGC[CAA/GTG]CCACAGCCACGCGACTAAGG	137
114-85/16D10/86	CTCAACGTAGCAAGTAATAA[T/G]ATACTGTCTATTTATGGTTA	138

115-N1/16E9/N2	AGACTTTCCCCATTCTCTTC[T/A]CCATCCACCGTCGAAACCCA	139
116-85/16H3/86-1	ACTTCGAAACTGTAAACCTA[A/T]ACTTTAAGAGTTTAGAGCTA	140
117-85/16H3/86-2	CACCATCGGAGAAAGAGGTA[C/T]TTCGAAACTGTAAACCTAAA	141
118-85/17A5/86	CTAAGGCGTCTCCTGAAGAA[A/G]TACAGAGAGTCGAAGAAGAT	142
119-85/17C7/86	CCGCGGACGACGCTTTCTTC[C/A]TCTGCTCCACCGCGAGCGCC	143
120-85/17F7/86	GAGGAGTAGTCTCCATGGCC[G/]AAGAAGAGCGTCGGAGACCTG	144
121-85/17G12/86	GAAGTTAGGGCTTCTAAGAT[C/T]AAGTTCGGCAAGGCTTTAAC	145
122-85/18A2/86	TCAAAACTAATATTTCTTTT[G/C]TTGATTGGTAATAAACAGGT	146
123-85/18A11/86	TTCCAGTGAAAAGGCATTGT[T/G]CTCCAAAATCTCGCTCTGCG	147
124-85/18F5/86	AAGCAGCTCTGACTTGAATG[C/A]GAGAGGTTAATCAGACTGTG	148
125-85/18H10/86-3	TAGATTGAAGCAATCAAGAA[G/A]ATCTCAGACTTCATCACCCA	149
126-85/19B3/86	GCATCCAACTCCAAGGATGA[/C]CCTGCCAAGGTGCTGCTAACT	150
127-85/19C8/86	GAGCTCAGGGATGGTGGATC[A/T]GACTACCTTGGAAAGGGTGT	151
128-N1/19F4/N2	TGGGGTTAGTCGAAATAGGT[A/T]AAATGCTTTGAGTATGTGTA	152
129-N1/19H1/N2	TACGCGCAGCACGGACTTGC[G/A]ACGCAAGCAATCGAGCTTTT	153
130-85/20B4/86-1	GAAGCCCATGGTACGGAGCG[G/A]GAGAGAGTCAAGTACTTGGG	154
131-N1/20B12/N2	AACGGGTCACTGCTAAATCA[T/A]AAGGATCACAAGGCTGGGAC	155
132-85/20C12/86	CTAGCCTACTTTGGGAAAAG[/T]TTCGTTATTGTTTTGTGTGG	156
133-85/20D2/86	GACTTCAAGGACTTCGCCGG[A/C]AAATGCTCCGACGCTGTCAA	157
134-85/20D3/86-2	GAGGAGGGCTACATGCAGCT[G/A]AAGAGGCTGAGGGGCTAAA	158
135-85/20D6/86-4	GATGTTCAACCTATGAAGAA[G/C]AAACACCGAGGACCAACGAG	159
136-85/20D6/86-5	CCATTAGTGAGGGAGCATGT[T/A]CCTGTCACATTGATGATTG	160

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137-85/20D6/86-8	AAACACATCGCCAAAGATCC[CG/AA]ACACTCGAGAAAGAGTGGAG	161
138-N1/20D8/N2	CTCATAGGCGATCTGGAGTA[T/G]GCAAATCGAATCTCCTCTCC	162
139-N1/20E1/N2	TGCACGCCTCACTTGTTCCT[T/A]CCAATCTGACATCAAGGATT	163
140-N1/20F1/N2-1	NGTGTTTTTGAGGTGAAAGC[A/T]ACAAATGGAGATACCTTTTT	164
141-N1/BoC-a2/N3-2	CCCGAGCCATTAGGACAAGA[T/C]GACTTGCCGTTTGACCAAAC	165
142-N1/BOC-A2/N3-1	CCCATCTCATCCTTTCTTGA[A/G]CCGTTGAATCAAGCTCCTGG	166
143-N1/BoC-a2/N3-3	TACATTCTCATTGGTTGGTT[C/A]TTGGGAAATAAAGTACCAAC	167
144-86/SC3	GCACGCGCTAGAGTTGTTGC[C]AGAAGGAATGAACAATCTGA	168
145-N3/SC3/N4-1	CTTGAGACCTATAGTCCTGT[A/T]GTTCGGTCCGCCACAGTTCG	169
146-N3/SC3/N5-1	CACAGTTCGTACAGTTCTTC[A/C]CATTGCCACTGTTATGCACT	170
147-N1/SC3/N3-1	GAAGGCGTCCACTATCTTGA[A/G]ACCTATAGTCCTGTTGTTCG	171
148-86/SC3/N4-1	TCCCGGAAATCTTGCTGAAA[A/C]CGTTTACCTGCGACAACCAG	172
149-B11/N5-1	ATGTCTTCAAAGTGCTCTGT[T]GCAACGCACGTCCGAACAAG	173